

**REMARKS**

These remarks are in response to the Office Action mailed October 21, 2004. The specification has been amended to identify parts A-E and A-G in figures 2 and 24, respectively. Applicants have canceled claim 36, without prejudice to Applicants' right to prosecute the canceled subject matter in any divisional, continuation, continuation-in-part, or other application. Claims 5-31 and 33-35 have been canceled as directed to a non-elected invention. Figures 14 and 27 have been amended to correct a sequence error as clearly evident by the publicly available sequences and to correct typographical errors. No new matter is believed to have been introduced.

Applicants acknowledge the Examiner's indication that claims 1-2, 32 and 37 are allowable.

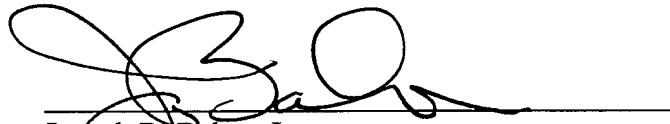
The rejections over claim 36 are now moot.

Please apply any other charges or credits to deposit account 06-1050.

Respectfully submitted,

Date: \_\_\_\_\_

10/28/04

  
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**IN THE DRAWINGS:**

Attached hereto are replacement sheets of drawings. Please substitute each of the drawings for the drawings currently on file.

The attached replacement sheets of drawings include changes to Figs. 14 and 27. Attached hereto are marked up copies of Figs. 14 and 27 showing the changes made in red ink. A clean copy of the figures are also included with the substitute figures.

The amendments to Fig. 14 correct the sequence number as evidence by counting of the respective amino acids. FIG. 27 corrects a typographical error in the sequence. The proper amino acid is recited in the sequence listing (See, SEQ ID NO:59) and as clearly evident by the published sequences available to one of skill in the art.



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Motif I			
RecJ_Tt	[73]	KRIRVHG DYADGLTGTA ILVRGLAALG	[100]
RecJ_Ec	[73]	TRII VVGDFDADGATSTALS VLAMRSLG	[100]
RecJ_Aa	[78]	KRIIIYGDYDVGITGTAILYRVLKLLG	[105]
RecJ_Hp	[47]	TEILVVG DYADGVISSA IMAKFFESLN	[74]
RecJ_Hi	[68]	QKII VVGDFDADGATSTALS VLALRQLG	[95]
PPX1_Sc	[30]	TICVGNESADMSIASA ITTYSYCOYIYN	[57]
PRUNE_Dm	<del>[37]</del> 38	HLVMGNESCDLSA VSAVTLAFVYAASS	<del>[60]</del> 65
		Motif II	Motif III
RecJ_Tt	[129]	SDLFLITVDCGITNHAELRE	[147] [153] VEVIVITPHHTPGK [165]
RecJ_Ec	[131]	AQLIVITVDNGISSHAGVEH	<del>[149]</del> 149 [155] IPVIVITPHHLPGD <del>[165]</del> 167
RecJ_Aa	[133]	GDFLIITVDNGTSAVEEIDQ	[151] [154] LETVVITPHHNVPP [166]
RecJ_Hp	[102]	APLIITVDNGINAFEAA RF	[120] [126] YTLIITPHHCLHH [138]
RecJ_Hi	[126]	VQLLMTVDNGVSSFDGVAF	[144] [150] IRVLVITPHHLPPE [162]
PPX1_Sc	[120]	ELNSYLVDNNDTPKNLKNY	[138] [141] NVVGIIDHFDLQ [153]
PRUNE_Dm	[88]	PLVCEMWD CRARVALPRRY	[106] [129] NVTEILDHRPLED [141]
		Motif IV	Specific Motif
RecJ_Tt	[210]	YADLA AVGTIADVAPLWG W	[228] [386] DLLLRYGGHKEAAGFAM [402]
RecJ_Ec	[226]	LLDLVALGT VADVVP L DAN	[244] [422] GMMLKFGGHAMAAGLSL [438]
RecJ_Aa	[215]	FLDLVALGLLADYMPVNPV	[233] [404] DMFLKWGGHOKAMGLTL [420]
RecJ_Hp	[189]	LLCLAGVATIADMMPLTFF	[207] [372] SLLGYGGHRQACGLSV [388]
RecJ_Hi	[219]	LLDLVALGTIADVVPLDQN	[237] [415] NMILKFGGHAMAAGLSI [431]
PPX1_Sc	[191]	IALLMGAILIDTSNMRRK	[209]
PRUNE_Dm	[183]	VAQLLHATIVLDITINFAPA	[201]

Tt : Thermus thermophilus HB8, Ec : Escherichia coli, Aa : Aquifex aeolicus,  
 Hp : Helicobacter pylori, Hi : Haemophilus influenzae Rd,  
 Sc : Saccharomyces cerevisiae, Dm : Drosophila melanogaster

FIG. 14



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	10	20	30	40	50	60
Tth	MRLLFRQRFNRLLALEAYRPPPGLSALVGANAQGKTSLLLGTHDA--LGGEVPLGL					
Eco	MSLRLRLTRDTRFNRLLIETADALSPGFENFLVGANGSGKTSVLEAIYTLGHGRIFRSLQII					
Ppu	MSLRLRLMTAVRNLLHPVTLLPSPRINILYVGANGSGKTSVLEAVHLLGLARISFRSTRLL					
Bsu	MYTQNLCELTSYRNYDHAELQFENXVNVITIGENAQGKTNLMEAIYVL SMAKSHRISND					
Mtu	MYVRLHGLRDFRSWACVDLELHPGRITVFVGPNGYGKTNLLEALWYSTTLGSHRVSAD					
Dra	MGDVRLLSALSTLNRYRNLLAPGTLNFPGLVITGTYGENGAGKTNLLEAAYLA-LTGQTDAPRI					
	M L L - -RN- L PG-- -G NG GKT LLEA- - R- -					
	70	80	90	100	110	120
Tth	ADLVRFGEELAWLHAEVETELG--AYRLEHRLGPGGREVLNGKR-VSLRTLWEIPGSV					
Eco	GRVIRHEQEAFLHGRLLQGEER-ETATGLTKDKQ-GDSKVRIDGTDGKVAELAHLMPMQ					
Ppu	NPVIOYQIAACTVFGVOLTEGGTSLNIGVSRERQ-GEFTLRID-----ALKPVF					
Bsu	KELIRWDKDYAKIEGRVMKQNG--AIPMOLVISKKGKKGKVNHIQQKLSQYVGALNTI					
Mtu	LPLIRVGTDRAVISTIVVNDGR-ECAYDL E IATG-RVNKAIRLNRSVSTRDVGVLRAV					
Dra	EQLIQAGETEAIVRADLQGGG--LSIQEIVGLGRGRRLKVDGVRARTGDLP--RGGAV					
	LIR -- A - V- A- -- G ---- -					
	130	140	150	160	170	180
Tth	LVSPLDLEAVLGPKEERRIAYLDRLLIAHFSRRYAAALLSAYEKAIRORNALLKAGG----					
Eco	LITPEGFTLLNGGPKYRRALFDWGCFFHNEPGFFTAWSNLTKRLKORNAARQVT--RY--					
Ppu	ERTLSELVELDGL-----					
Bsu	MFAPEDLNLVKGSPIQVRRRIFLDMEIGQVSPVYLHDLISLYOKILSORNHFLKLOLTRKQTD					
Mtu	LFAPEDLGLVRGDPADRRRIYLDLALVRRPATAAVRAEYERVLQRRTALLKLSVPGARYRG					
Dra	WIRPEDSELVFGPPSGRRRIAYLDSLLSRLSARYGEQLSRYERTVSORNALRLGGEE-----					
	--PEDL LV G P RR -LD - - S Y-- L QRNAL-					
	190	200	210	220	230	240
Tth	-----EGLSAWDRELARYGDEIVALLRRFLRRIFAP-----ILREVHAALAAKEAGLR					
Eco	-----EQLRPWDKELIPLAEQISTWRAEYSAGLAADMADTCKQFLPEF-SLTESFORGWE					
Ppu	-----LTLSSYIRGWD					
Bsu	R-----TMDVLTDOVEVAAKVWVKRLQFTAQLEKWAQPIHAGISRGLEELTLKYHTALD					
Mtu	DRGVFDTLLDLDWSRLAEHGAELVAARRIDLVNQLAPEVKKAYQLAPESRSASIGYRASMD					
Dra	-----WAMHVWDVLLKLGTEIMLRFRRLTRLD-----ELAREANAQLGSRKTLA					
	L WD L --- R --					
	250	260	270	280	290	300
Tth	EETAGEG-VLRAIEASRAE-----ERE--RGOTLVGPHRDDLVLEGRPAHRFAISR					
Eco	KE--TE-----YAEVLERNFE-----RDRO--LTYYAHGPHKADLRIRADGAPVEDTLR					
Ppu	KD--RE-----LOEVLASSLL-----RDQO--MGHTQAGPORADLRRLTAGNNADILSR					
Bsu	VSDPLDLISKIGDSYQEAFSK-----LREKEIERGVITLSGPHRDDVLFYVNGRDVQTYGSQ					
Mtu	VTGPSEQSDIDROTLLAARLLAALAARRDAELERGVCLVGPHRDDLIIRLGDQPAKGFAISH					
Dra	LTLTES--TSPETYAADLRG--RRAEELARGSTVITGPHRDDLLLTIGDFPASDYASR					
	- - - - A - R--E RG T- GPHRDDL-- LG PA - SR					
	310	320	330	340	350	360
Tth	GEAKTLALALRLAEHRLGHHGEPILLLVIDEWGEELDEARRRAVLAYAQALPOATLAGL					
Eco	GOLKLLMCAALRLAQGEFLTRESGRRCLYLIDDFASELDDEIRRGLLASRLKATQSQVFSVA					
Ppu	GOQKLLVVCALRLTAQGHVLSQARRGHCILYLVDDLPSELDDOHRRLALCRLLELRCCQSSPV					
Bsu	GOQRITLALSLKLAIEDLIIHEEIGEPILLLDDVLSSELDDYRQSHLLHTIIG-RVOITFVTI					
Mtu	GEAWSLAVIALRLAAYQLTRVD--GGEPVILLDDVFAELDMRRRIALATAAES-AEQVLVTA					
Dra	GEGRTVALIALRLAELLLREKFGEDPVLLLLDDFTAEIDPHRRQYLLDLAASVPOAIVTGT					
	G- ---A-ALRLA- LL - G P-LL-DD -ELD- RR- L - - Q- -					
	370	380	390			
Tth	EAPPGVVPCSVVRIGVVLCPGA			343		
Eco	ISAHVIDMSDENSKMFTVEKGKITD			357		
Ppu				233		
Bsu	TSVDGTDHETLRQAGMFRVQNGALVK			370		
Mtu	AVLEDIPAGWDARRVHIDVRADDTGSM SVLP			385		
Dra	ELAPGAALTLRQAGRFTPVADEEMQAEGTA			359		

Tth: Thermus thermophilus HB8  
Eco: Escherichia coli  
Ppu: Pseudomonas putida  
Bsu: Bacillus subtilis  
Mtu: Mycobacterium tuberculosis  
Dra: Deinococcus radiodurans

FIG. 27